Exhibit E

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<!--StartFragment-->RESULT 2
ABT07740
ID    ABT07740 standard; DNA; 2119 BP.
XX
AC    ABT07740;
XX
DT    14-NOV-2002  (first entry)
XX
DE    Breast cancer-associated gene sequence 48.
XX
KW    Gene; ds; breast cancer; breast cancer-associated gene sequence;
KW    drug development; pharmacogenetics; biosensor development.
XX
OS    Unidentified.
XX
FN    WO200259377-A2.
XX
PD    01-AUG-2002.
XX
PF    24-JAN-2002; 2002WO-US002242.
XX
PR    24-JAN-2001; 2001US-0263965P.
PR    02-FEB-2001; 2001US-0265928P.
PR    09-APR-2001; 2001US-00829472.
PR    09-APR-2001; 2001US-0282698P.
PR    04-MAY-2001; 2001US-0288590P.
PR    29-MAY-2001; 2001US-0294443P.
XX
PA    (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI    Mack DH, Gish KC, Afar D;
XX
DR    WPI; 2002-583738/62.
DR    N-PSDB; ABJ05583.
XX
PT    Detecting a breast cancer-associated transcript in a patient's cell,
PT    useful for diagnosing breast cancer, comprises contacting a biological
PT    sample with a polynucleotide that selectively hybridizes with breast
PT    cancer nucleic acids.
XX
PS    Claim 9; Page 388-389; 414pp; English.
XX
CC    The invention comprises a method of detecting a breast cancer-associated
CC    transcript in a cell from a patient. The method of the invention involves
CC    contacting a biological sample from the patient with a nucleotide that
CC    hybridises to one of the 69 breast cancer-associated gene sequences shown
CC    in the specification. The method of the invention is useful in the
CC    diagnosis or prognosis of breast cancer, and for detecting genes that are
CC    up or down-regulated in breast cancer cells. Genes identified by the
CC    method of the invention can be used in diagnostic purposes and also as
CC    targets for screening for therapeutic compounds that modulate breast
CC    cancer (e.g. hormones or antibodies). Identification of genes that are
CC    over or under expressed in breast cancer can additionally provide high-
CC    resolution, high-sensitivity datasets which can be used in the areas of
CC    diagnostics, therapeutics, drug development, pharmacogenetics, protein
CC    structure and biosensor development. DNA sequences ABT07693 - ABT07761
CC    represent the 69 breast cancer-associated gene sequences of the invention
XX
SQ    Sequence 2119 BP; 646 A; 389 C; 492 G; 592 T; 0 U; 0 Other;

      Query Match            100.0%; Score 2119; DB 6; Length 2119;
      Best Local Similarity  100.0%; Pred. No. 0;
      Matches 2119; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Qy          1 GGCACGAGTAGGGGTGGCGGGTCAGTGCTGCTCGGGGGCTTCTCCATCCAGGTCCCTGGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCACGAGTAGGGGTGGCGGGTCAGTGCTGCTCGGGGGCTTCTCCATCCAGGTCCCTGGA 60

Qy         61 GTTCCTGGTCCCTGGAGCTCCGCACTTGGCGCGCAACCTGCGTGAGGCAGCGCGACTCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCCTGGTCCCTGGAGCTCCGCACTTGGCGCGCAACCTGCGTGAGGCAGCGCGACTCTG 120

Qy        121 GCGACTGGCCGGCCATGCCTTCCCGGGCTGAGGACTATGAAGTGTTGTACACCATTGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGACTGGCCGGCCATGCCTTCCCGGGCTGAGGACTATGAAGTGTTGTACACCATTGGCA 180
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Qy    181  CAGGCTCCTACGGCCGCTGCCAGAAGATCCGGAGGAAGAGTGATGGCAAGATATTAGTTT  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CAGGCTCCTACGGCCGCTGCCAGAAGATCCGGAGGAAGAGTGATGGCAAGATATTAGTTT  240

Qy    241  GGAAAGAACTTGACTATGGCTCCATGACAGAAGCTGAGAAACAGATGCTTGTTTCTGAAG  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  GGAAAGAACTTGACTATGGCTCCATGACAGAAGCTGAGAAACAGATGCTTGTTTCTGAAG  300

Qy    301  TGAATTTGCTTCGTGAACTGAAACATCCAAACATCGTTCGTTACTATGATCCGGATTATTG  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  TGAATTTGCTTCGTGAACTGAAACATCCAAACATCGTTCGTTACTATGATCCGGATTATTG  360

Qy    361  ACCCGGACCAATACAACACTGTACATTGTAATGGAATATTGTGAAGGAGGGGATCTGGCTA  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  ACCCGGACCAATACAACACTGTACATTGTAATGGAATATTGTGAAGGAGGGGATCTGGCTA  420

Qy    421  GTGTAATTACAAACGGAACCAAGGAAAGGCAATACTTAGATGAAGAGTTTGTTCTTCGAG  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  GTGTAATTACAAACGGAACCAAGGAAAGGCAATACTTAGATGAAGAGTTTGTTCTTCGAG  480

Qy    481  TGATGACTCAGTTGACTCTGGCCCTGAAGGAATGCCACAGACGAAGTGATGGTGGTCATA  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TGATGACTCAGTTGACTCTGGCCCTGAAGGAATGCCACAGACGAAGTGATGGTGGTCATA  540

Qy    541  CCGTATTGCATCGGGATCTTAAACCAGCCAATGTTTTCCTGGATGGCAAGCAAAACGTCA  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  CCGTATTGCATCGGGATCTTAAACCAGCCAATGTTTTCCTGGATGGCAAGCAAAACGTCA  600

Qy    601  AGCTTGGAGACTTTGGGCTAGCTAGAATATTAAACCATGACACGAGTTTTGCAAAAACAT  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  AGCTTGGAGACTTTGGGCTAGCTAGAATATTAAACCATGACACGAGTTTTGCAAAAACAT  660

Qy    661  TTGTTGGCACACCTTATTACATGTCTCCTGAACAAATGAATCGCATGTCCTACAATGAGA  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  TTGTTGGCACACCTTATTACATGTCTCCTGAACAAATGAATCGCATGTCCTACAATGAGA  720

Qy    721  AATCAGATATCTGGTCATTGGGCTGCTTGCTGTATGAGTTATGTGCATTAATGCCTCCAT  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  AATCAGATATCTGGTCATTGGGCTGCTTGCTGTATGAGTTATGTGCATTAATGCCTCCAT  780

Qy    781  TTACAGCTTTTAGCCAGAAAGAACTCGCTGGGAAAATCAGAGAAGGCAAATTCAGGCGAA  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  TTACAGCTTTTAGCCAGAAAGAACTCGCTGGGAAAATCAGAGAAGGCAAATTCAGGCGAA  840

Qy    841  TTCCATACCGTTACTCTGATGAATTGAATGAAATTATTACGAGGATGTTAAACTTAAAGG  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TTCCATACCGTTACTCTGATGAATTGAATGAAATTATTACGAGGATGTTAAACTTAAAGG  900

Qy    901  ATTACCATCGCACCTTCTGTTGAAGAAATTCTTGAGAACCCTTTAATAGCAGATTTGGTTG  960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  ATTACCATCGCACCTTCTGTTGAAGAAATTCTTGAGAACCCTTTAATAGCAGATTTGGTTG  960

Qy    961  CAGACGAGCAAAGAAGAAATCTTGAGAGAAGAGGGCGACAATTAGGAGAGCCAGAAAAAT  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  CAGACGAGCAAAGAAGAAATCTTGAGAGAAGAGGGCGACAATTAGGAGAGCCAGAAAAAT  1020

Qy   1021  CGCAGGAATTCCAGCCCTGTATTGAGTGGAGCTGAAACTGAAGGAAATTCAGTTACAGGAGC  1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  CGCAGGAATTCCAGCCCTGTATTGAGTGGAGCTGAAACTGAAGGAAATTCAGTTACAGGAGC  1080

Qy   1081  GAGAGCGAGCTCTCAAAGCAAGAGAAGAAAGATTGGAGCAGAAAGAACAGGAGCTTTGTG  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  GAGAGCGAGCTCTCAAAGCAAGAGAAGAAAGATTGGAGCAGAAAGAACAGGAGCTTTGTG  1140

Qy   1141  TTCGTGAGAGGACTAGCAGAGGACAAACTGGCTACAGCAGAAAATCTGTTGAAGAACTACA  1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  TTCGTGAGAGGACTAGCAGAGGACAAACTGGCTACAGCAGAAAATCTGTTGAAGAACTACA  1200

Qy   1201  GCTTGCTAAAGGAACGGAAGTTCCTGTCTCTGGCAAGTAATCCAGAACTTCTTAATCTTC  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  GCTTGCTAAAGGAACGGAAGTTCCTGTCTCTGGCAAGTAATCCAGAACTTCTTAATCTTC  1260

Qy   1261  CATCCTCAGTAATTAAGAAGAAAGTTCATTTCAGTGGGGAAAGTAAAGAGAACATCATGA  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  CATCCTCAGTAATTAAGAAGAAAGTTCATTTCAGTGGGGAAAGTAAAGAGAACATCATGA  1320
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Qy    1321 GGAGTGAGAATTCTGAGAGTCAGCTCACATCTAAGTCCAAGTGCAAGGACCTGAAGAAAA 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GGAGTGAGAATTCTGAGAGTCAGCTCACATCTAAGTCCAAGTGCAAGGACCTGAAGAAAA 1380

Qy    1381 GGCTTCACGCTGCCCAGCTGCGGGCTCAAGCCCTGTCAGATATTGAGAAAAATTACCAAC 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GGCTTCACGCTGCCCAGCTGCGGGCTCAAGCCCTGTCAGATATTGAGAAAAATTACCAAC 1440

Qy    1441 TGAAAAGCAGACAGATCCTGGGCATGCGCTAGCCAGGTAGAGAGACACAGAGCTGTGTAC 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 TGAAAAGCAGACAGATCCTGGGCATGCGCTAGCCAGGTAGAGAGACACAGAGCTGTGTAC 1500

Qy    1501 AGGATGTAATATTACCAACCTTTAAAGACTGATATTCAAATGCTGTAGTGTTGAATACTT 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGGATGTAATATTACCAACCTTTAAAGACTGATATTCAAATGCTGTAGTGTTGAATACTT 1560

Qy    1561 GGCCCCATGAGCCATGCCTTTCTGTATAGTACACATGATATTTCGGAATTGGTTTTACTG 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GGCCCCATGAGCCATGCCTTTCTGTATAGTACACATGATATTTCGGAATTGGTTTTACTG 1620

Qy    1621 TTCTTCAGCAACTATTGTACAAAATGTTCACATTTAATTTTTCTTTCTTCTTTTAAGAAC 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 TTCTTCAGCAACTATTGTACAAAATGTTCACATTTAATTTTTCTTTCTTCTTTTAAGAAC 1680

Qy    1681 ATATTATAAAAAGAATACTTTCTTGGTTGGGCTTTTAATCCTGTGTGTGATTACTAGTAG 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 ATATTATAAAAAGAATACTTTCTTGGTTGGGCTTTTAATCCTGTGTGTGATTACTAGTAG 1740

Qy    1741 GAACATGAGATGTGACATTCTAAATCTTGGGAGAAAAAATAATATTAGGAAAAAAATATT 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 GAACATGAGATGTGACATTCTAAATCTTGGGAGAAAAAATAATATTAGGAAAAAAATATT 1800

Qy    1801 TATGCAGGAAGAGTAGCACTCACTGAATAGTTTTAAATGACTGAGTGGTATGCTTACAAT 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 TATGCAGGAAGAGTAGCACTCACTGAATAGTTTTAAATGACTGAGTGGTATGCTTACAAT 1860

Qy    1861 TGTCATGTCTAGATTTAAATTTTAAGTCTGAGATTTTAAATGTTTTTGAGCTTAGAAAAC 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 TGTCATGTCTAGATTTAAATTTTAAGTCTGAGATTTTAAATGTTTTTGAGCTTAGAAAAC 1920

Qy    1921 CCAGTTAGATGCAATTTGGTCATTAATACCATGACATCTTGCTTATAAATATTCCATTGC 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 CCAGTTAGATGCAATTTGGTCATTAATACCATGACATCTTGCTTATAAATATTCCATTGC 1980

Qy    1981 TCTGTAGTTCAAATCTGTTAGCTTTGTGAAAATTCATCACTGTGATGTTTGTATTCTTTT 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 TCTGTAGTTCAAATCTGTTAGCTTTGTGAAAATTCATCACTGTGATGTTTGTATTCTTTT 2040

Qy    2041 TTTTTTTCTGTTTAACAGAATATGAGCTGTCTGTCATTTACCTACTTCTTTCCCACTAAA 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 TTTTTTTCTGTTTAACAGAATATGAGCTGTCTGTCATTTACCTACTTCTTTCCCACTAAA 2100

Qy    2101 TAAAAGAATTCTTCAGTTA 2119
           |||||||||||||||||||
Db    2101 TAAAAGAATTCTTCAGTTA 2119
<!--EndFragment-->
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